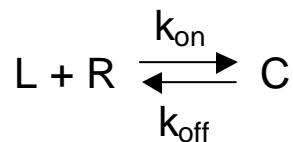


- From your ITC experiments, you have determined that a particular protein-small molecule binding interaction has a ΔG of -10.49 kcal/mol (at 25°C).
 - Using this information, calculate the off rate (k_{off}) assuming that k_{on} is 10^5 L/mol·sec.
 - In an SPR experiment, what is the characteristic time constant $\tau_{1/2}$ given $[P]_o = 100$ nanomolar. How does this time change with $[P]_o$ decreasing to 10 nanomolar?
 - Calculate fractional saturation at equilibrium for these 2 conditions?
- Can you use $\tau_{1/2}$ to estimate peak width (the width of each of the “spikes”) in an ITC experiment? If not, why not?
- As developed in class, $k_{\text{obs}} = k_{\text{on}}[L]_o + k_{\text{off}}$. Perhaps not surprisingly, increasing k_{on} or $[L]_o$ results in more rapid approach to equilibrium (k_{obs} increases and $\tau_{1/2}$ decreases). Interestingly, increasing the off rate (k_{off}) also results in a faster approach to equilibrium. Show that this is the case with 3 different values of k_{off} while keeping k_{on} and $[L]_o$ constant. Explain why k_{off} has this effect on k_{obs} .
- To estimate the activation energy (E_a), you perform SPR experiments at 25°C and at 5°C. For this particular system, the rate constant decreases by 50% when the temperature is decreased from 25°C to 5°C. Calculate E_a (assume E_a constant over this range).
- Download the code hw3.m and C_function.m. This code creates data for C(t) for the following reaction.



Please modify this code to fit the model equation for C(t) (given in the file C_function.m) to the data to obtain the parameters kon and koff. The only line missing from the hw3.m code is the line that solves for the variable “fit_k” using the nlinfit function. This position for this line is marked with “%% % % % %”. Write the missing line to fit for kon and koff, and turn in the missing line with your solution along with the final plot the code produces of the fitted solution plotted on top of the data.

- Download ODEexample.m and ODEexample_equations.m from the MATLAB section of the “Study Materials” part of the website. The system we want to model is slightly different from the one coded up in this example, and is pictured below. Our receptor can still bind our ligand to form complex as before. However, the receptor can also bind to a second ligand to form a second type of complex. Therefore, the two ligands are in competition for the receptor.

Please modify this code to simulate the new system, with initial concentrations of 2M for L2 and 0M for C2. The k1on and k1off rate constants should be the same as the kon and koff rate constants in the original example and the L1 and C1 initial concentrations are

the same as those for L and C in the original example. Play with different values for the k_{2on} and k_{2off} rate constants.

L2 is really a drug we are developing to combat against disease caused by C1. Can you come up with a set of k_{2on} and k_{2off} rate constants that causes $[C2] > [C1]$ by the end of the simulation? If so, please make a plot of all 5 components versus time, with labels. If not, what should we modify about our L2 drug so that $[C2] > [C1]$ by the end of the simulation? Note, you cannot change anything about the L1 reaction because it is the native reaction in the cell. Attach a plot of all 5 components versus time, with labels, showing that your method works.

